

SEQUENCE LISTING

<110> The Government of the United States

<120> Bovine Adeno-Associated Viral (BAAV)
Vector and Uses Thereof

<130> 14014.0417P1

<140> Unassigned

<141> 2004-12-06

<150> 60/526,786

<151> 2003-12-04

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 4694

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic
construct

<400> 1

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<210> 2

<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic construct

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gaatgtgacg agtgtgaata tttgaatcgg ggcaaaaatg gctgtatctt tcataatgct      1740
acacattgtc aaatttgtca cgctgttcct ccatgggaaa aggaaaatgt gtcagatttt      1800
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<210> 3

<211> 610

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic construct

<400> 3

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Met Ala Thr Phe Tyr Glu Val Ile Val Arg Val Pro Phe Asp Val Glu
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Glu His Leu Pro Gly Ile Ser Asp Asn Phe Val Asp Trp Val Thr Gly
 20          25          30
Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Ile
 35          40          45
Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
 50          55          60
Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
 65          70          75          80
Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
 85          90          95
Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
 100         105         110
Ala Gln Leu Val Lys Val Val Phe Gln Asn Ile Glu Pro Arg Ile Asn
 115         120         125
Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
 130         135         140
Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
 145         150         155         160

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Glu Leu Gln Trp Ala Trp Thr Asn Leu Glu Glu Tyr Lys Leu Ala Ala
 165 170 175
 Leu Asn Leu Glu Arg Lys Arg Leu Val Ala Gln Phe Gln Leu Glu
 180 185 190
 Ser Ser Gln Arg Ser Gln Glu Ala Ser Ser Gln Arg Asp Val Ser Ala
 195 200 205
 Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val
 210 215 220
 Ser Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln
 225 230 235 240
 Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg
 245 250 255
 Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys Ile Met Ser Leu
 260 265 270
 Thr Lys Ser Ala Ser Asp Tyr Leu Val Gly Gln Thr Val Pro Glu Asp
 275 280 285
 Ile Ser Glu Asn Arg Ile Trp Gln Ile Phe Asp Leu Asn Gly Tyr Asp
 290 295 300
 Pro Ala Tyr Ala Gly Ser Val Leu Tyr Gly Trp Cys Thr Arg Ala Phe
 305 310 315 320
 Gly Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys
 325 330 335
 Thr Asn Ile Ala Glu Ala Ile Ser His Thr Val Pro Phe Tyr Gly Cys
 340 345 350
 Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Glu Lys
 355 360 365
 Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Ser Lys Val Val Glu
 370 375 380
 Pro Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg Val Asp Gln Lys
 385 390 395 400
 Cys Lys Ser Ser Val Gln Val Asp Ser Thr Pro Val Ile Ile Thr Ser
 405 410 415
 Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu
 420 425 430
 His Gln Gln Pro Leu Glu Asp Arg Met Phe Arg Phe Glu Leu Met Arg
 435 440 445
 Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
 450 455 460
 Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
 465 470 475 480
 Met Val Pro Lys Lys Val Ala Gly Thr Glu Arg Ala Glu Thr Ser Arg
 485 490 495
 Lys Arg Pro Leu Asp Asp Val Thr Asn Thr Asn Tyr Lys Ser Pro Glu
 500 505 510
 Lys Arg Ala Arg Leu Ser Val Val Pro Glu Thr Pro Arg Ser Ser Asp
 515 520 525
 Val Pro Val Glu Pro Ala Pro Leu Arg Pro Leu Asn Trp Ser Ser Arg
 530 535 540
 Tyr Glu Cys Arg Cys Asp Tyr His Ala Lys Phe Asp Ser Val Thr Gly
 545 550 555 560
 Glu Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys Asn Gly Cys Ile
 565 570 575
 Phe His Asn Ala Thr His Cys Gln Ile Cys His Ala Val Pro Pro Trp
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 Glu Lys Glu Asn Val Ser Asp Phe Asn Asp Phe Asp Asp Cys Asn Lys
 595 600 605
 Glu Gln
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<210> 4

<211> 1173

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic construct

<400> 4

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gccgcgcttg acaacgcgtc aaaaattatg agtctgacca aatctgcctc agactatctc      180
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gaagccatct ctcacaccgt gcccttttat ggctgtgtga actggactaa tgagaacttt      420
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aaggtggtgg aacccgccaa ggccatcttg ggggggtcta gactacgagt ggatcaaaaa      540
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gatgacgtca ccaataccaa ctataaaagt ccggagaagc gggcccggct ctcagttggt      900
cctgagacgc ctgcgagttc agacgtgcct gtagagcccg ctctctgcg acctctcaac      960
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<210> 5

<211> 390

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic construct

<400> 5

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Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
      20              25              30
Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
      35              40              45
Ile Met Ser Leu Thr Lys Ser Ala Ser Asp Tyr Leu Val Gly Gln Thr
      50              55              60
Val Pro Glu Asp Ile Ser Glu Asn Arg Ile Trp Gln Ile Phe Asp Leu
      65              70              75              80
Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Leu Tyr Gly Trp Cys
      85              90              95
Thr Arg Ala Phe Gly Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
      100             105             110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ser His Thr Val Pro
      115             120             125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130             135             140
Cys Val Glu Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Ser
      145             150             155             160
Lys Val Val Glu Pro Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg
      165             170             175

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Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Val	Gln	Val	Asp	Ser	Thr	Pro	Val
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		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Glu	Asp	Arg	Met	Phe	Arg	Phe
		210				215					220				
Glu	Leu	Met	Arg	Arg	Leu	Pro	Pro	Asp	Phe	Gly	Lys	Ile	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Ala	Trp	Ala	Lys	Val	Asn	Gln	Val	Pro	Val
				245					250					255	
Thr	His	Glu	Phe	Met	Val	Pro	Lys	Lys	Val	Ala	Gly	Thr	Glu	Arg	Ala
			260					265					270		
Glu	Thr	Ser	Arg	Lys	Arg	Pro	Leu	Asp	Asp	Val	Thr	Asn	Thr	Asn	Tyr
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Lys	Ser	Pro	Glu	Lys	Arg	Ala	Arg	Leu	Ser	Val	Val	Pro	Glu	Thr	Pro
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Arg	Ser	Ser	Asp	Val	Pro	Val	Glu	Pro	Ala	Pro	Leu	Arg	Pro	Leu	Asn
305					310					315					320
Trp	Ser	Ser	Arg	Tyr	Glu	Cys	Arg	Cys	Asp	Tyr	His	Ala	Lys	Phe	Asp
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Ser	Val	Thr	Gly	Glu	Cys	Asp	Glu	Cys	Glu	Tyr	Leu	Asn	Arg	Gly	Lys
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Asn	Gly	Cys	Ile	Phe	His	Asn	Ala	Thr	His	Cys	Gln	Ile	Cys	His	Ala
		355					360					365			
Val	Pro	Pro	Trp	Glu	Lys	Glu	Asn	Val	Ser	Asp	Phe	Asn	Asp	Phe	Asp
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Asp	Cys	Asn	Lys	Glu	Gln										
385					390										

<210> 6

<211> 2211

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic construct

<400> 6

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gccagcgaca	ccttcaacgg	attctccacc	ccctggggat	actttgactt	taaccgcttc	840
cactgccact	tctcgccaag	agactggcaa	aggctcatca	acaaccactg	gggactgcgc	900
cccaaaagca	tgcaagtccg	catcttcaac	atccaagtta	aggaggtcac	gacgtctaac	960
ggggagacga	cgtatccaa	caacctcacc	agcacggtcc	agatctttgc	ggacagcacg	1020
tacgagctcc	cgtacgtgat	ggatgcaggt	caggagggca	gcttgccctc	tttccccaac	1080
gacgtgttca	tgggtgcctca	gtacgggtac	tgcggtactg	taaccggagg	cagctctcaa	1140
aaccagacag	acagaaatgc	cttctactgt	ctggagtact	ttcccagcca	gatgctgaga	1200
accggaacaa	acttttgagat	ggtgtacaag	tttgaaaacg	tgcccttcca	ctccatgtac	1260
gctcacagcc	agagcctgga	taggctgatg	aacccgctgc	tggaccagta	cctgtggggag	1320

```

ctccagtcta ccacctctgg aggaactctc aaccagggca attcagccac caactttgcc 1380
aagctgacca aaacaaactt ttctggctac cgcaaaaact ggctcccggg gcccatgatg 1440
aagcagcaga gattctccaa gactgccagt caaaactaca agattcccca gggaagaaac 1500
aacagtctgc tccattatga gaccagaact accctcgacg gaagatggag caattttgcc 1560
ccgggaacgg ccatggcaac cgcagccaac gacgccaccg acttctctca ggcccagctc 1620
atctttgctg ggcccaacat caccggcaac accaccacag atgccaataa cctgatgttc 1680
acttcagaag atgaacttag ggccaccaac ccccgggaca ctgacctgtt tggccacctg 1740
gcaaccaacc agcaaaacgc caccaccgtt cctaccgtag acgacgtgga cggagtcggc 1800
gtgtaccctg gaatggtgtg gcaggacaga gacatttact accaagggcc catttggggc 1860
aaaattccac acacggatgg acactttcac ccgtctctc tcattggcgg atttggactg 1920
aaaagcccg ctcacacaaat attcatcaaa aacactcctg taccgcca tcccgcacg 1980
accttctctc cggccagaat caacagcttc atcaccag acagcaccg acaggtggct 2040
gtcaaaatag aatgggaaat ccagaaggag cggccaaga gatggaaccc agaggtccag 2100
ttcacgtcca actacggagc acaggactcg cttctctggg ctcccgacaa cgccggagcc 2160
tacaagagc ccaggggccat tggatcccga tacctacca accaccteta g 2211

```

<210> 7

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic construct

<400> 7

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Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Ser Ile Gly Asp
1      5      10      15
Gly Phe Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20      25      30
Ala Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35      40      45
Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Asp Pro Val
50      55      60
Asn Phe Ala Asp Glu Val Ala Arg Glu His Asp Leu Ser Tyr Gln Lys
65      70      75      80
Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85      90      95
Ala Glu Phe Gln Glu Lys Leu Ala Ser Asp Thr Ser Phe Gly Gly Asn
100     105     110
Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
115     120     125
Gly Leu Val Glu Thr Pro Asp Lys Thr Ala Pro Ala Ala Lys Lys Arg
130     135     140
Pro Leu Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145     150     155     160
Lys Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Asp Asp Glu
165     170     175
Pro Gly Ala Gly Asp Gly Pro Pro Pro Glu Gly Pro Ser Ser Gly Ala
180     185     190
Met Ser Thr Glu Thr Glu Met Arg Ala Ala Ala Gly Gly Asn Gly Gly
195     200     205
Asp Ala Gly Gln Gly Ala Glu Gly Val Gly Asn Ala Ser Gly Asp Trp
210     215     220
His Cys Asp Ser Thr Trp Ser Glu Ser His Val Thr Thr Thr Ser Thr
225     230     235     240
Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu
245     250     255
Gly Ser Ser Asn Ala Ser Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp
260     265     270

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Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
 275 280 285
 Trp Gln Arg Leu Ile Asn Asn His Trp Gly Leu Arg Pro Lys Ser Met
 290 295 300
 Gln Val Arg Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn
 305 310 315 320
 Gly Glu Thr Thr Val Ser Asn Asn Leu Thr Ser Thr Val Gln Ile Phe
 325 330 335
 Ala Asp Ser Thr Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu
 340 345 350
 Gly Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr
 355 360 365
 Gly Tyr Cys Gly Leu Val Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp
 370 375 380
 Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
 385 390 395 400
 Thr Gly Asn Asn Phe Glu Met Val Tyr Lys Phe Glu Asn Val Pro Phe
 405 410 415
 His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
 420 425 430
 Leu Leu Asp Gln Tyr Leu Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly
 435 440 445
 Thr Leu Asn Gln Gly Asn Ser Ala Thr Asn Phe Ala Lys Leu Thr Lys
 450 455 460
 Thr Asn Phe Ser Gly Tyr Arg Lys Asn Trp Leu Pro Gly Pro Met Met
 465 470 475 480
 Lys Gln Gln Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro
 485 490 495
 Gln Gly Arg Asn Asn Ser Leu Leu His Tyr Glu Thr Arg Thr Thr Leu
 500 505 510
 Asp Gly Arg Trp Ser Asn Phe Ala Pro Gly Thr Ala Met Ala Thr Ala
 515 520 525
 Ala Asn Asp Ala Thr Asp Phe Ser Gln Ala Gln Leu Ile Phe Ala Gly
 530 535 540
 Pro Asn Ile Thr Gly Asn Thr Thr Thr Asp Ala Asn Asn Leu Met Phe
 545 550 555 560
 Thr Ser Glu Asp Glu Leu Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu
 565 570 575
 Phe Gly His Leu Ala Thr Asn Gln Gln Asn Ala Thr Thr Val Pro Thr
 580 585 590
 Val Asp Asp Val Asp Gly Val Gly Val Tyr Pro Gly Met Val Trp Gln
 595 600 605
 Asp Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
 625 630 635 640
 Lys Ser Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655
 Asn Pro Ala Thr Thr Phe Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr
 660 665 670
 Gln Tyr Ser Thr Gly Gln Val Ala Val Lys Ile Glu Trp Glu Ile Gln
 675 680 685
 Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
 690 695 700
 Tyr Gly Ala Gln Asp Ser Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala
 705 710 715 720
 Tyr Lys Glu Pro Arg Ala Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
 725 730 735

<210> 8

<211> 1803

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic construct

<400> 8

```

acggcgccctg cggcaaaaaa gaggcctcta gagcagagtc ctcaagagcc agactcctcg      60
agcggagttg gcaagaaagg caaacagcct gccagaaaga gactcaactt tgacgacgaa      120
cctggagccg gagacgggccc tccccagaa ggaccatctt ccggagctat gtctactgag      180
actgaaatgc gtgcagcagc tggcggaat ggtggcgatg cgggacaagg tgccgagggg      240
gtgggtaatg cctccgggtga ttggcattgc gattccactt ggtcagagag ccacgtcacc      300
accacctcaa cccgcacctg ggtcctgccg acctacaaca accacctgta cctgcggctc      360
ggctcgagca acgccagcga caccttcaac ggattctcca cccctggggg atactttgac      420
tttaaccgct tccactgcca cttctcgcca agagactggc aaagggtcat caacaaccac      480
tggggactgc gccccaaaaa catgcaagtc cgcattctca acatccaagt taaggaggtc      540
acgacgtcta acggggagac gaccgtatcc aacaacctca ccagcacggg ccagatcttt      600
gcggacagca cgtacgagct cccgtacgtg atggatgcag gtcaggaggg cagcttgccct      660
cctttccccc acgacgtgtt catggtgcct cagtacgggt actgcggact ggtaaccgga      720
ggcagctctc aaaaccagac agacagaaat gccttctact gtctggagta ctttcccagc      780
cagatgctga gaaccggaaa caactttgag atggtgtaca agtttgaaaa cgtgcccttc      840
cactccatgt acgtcacag ccagagcctg gataggctga tgaaccgct gctggaccag      900
tacctgtggg agctccagtc taccacctct ggaggaactc tcaaccaggg caattcagcc      960
accaactttg ccaagctgac caaaacaaac ttttctggct accgcaaaaa ctggctcccc      1020
gggcccattg tgaagcagca gagattctcc aagactgcca gtcaaaaacta caagattccc      1080
caggggaaga acaacagtct gctccattat gagaccagaa ctaccctcga cggaagatgg      1140
agcaattttg ccccggggaa ggccatggca accgcagcca acgacgccac cgacttctct      1200
caggcccagc tcacttttgc ggggcccacc atcaccggca acaccaccac agatgccaat      1260
aacctgatgt tcacttcaga agatgaactt agggccacca acccccggga cactgacctg      1320
tttggccacc tggcaaccaa ccagcaaaac gccaccaccg ttctaccgt agacgacgtg      1380
gacggagtcg gcgtgtaccc gggaatggtg tggcaggaca gagacattta ctaccaaggg      1440
cccatttggg ccaaaattcc acacacggat ggacacttcc acccgtctcc tctcattggc      1500
ggatttggac tgaaaagccc gcctccacaa atattcatca aaaacactcc tgtaccgcc      1560
aatcccgcaa cgaccttctc tccggccaga atcaacagct tcacacacca gtacagcacc      1620
ggacaggtgg ctgtcaaaat agaatgggaa atccagaagg agcgggtcaa gagatggaa      1680
ccagaggtcc agttcacgtc caactacgga gcacaggact cgcttctctg ggctcccgac      1740
aacgccggag cctacaaaaga gccacgggccc attggatccc gatacctcac caaccacctc      1800
tag                                                                 1803

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<210> 9

<211> 600

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic construct

<400> 9

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Thr Ala Pro Ala Ala Lys Lys Arg Pro Leu Glu Gln Ser Pro Gln Glu
 1           5           10           15
Pro Asp Ser Ser Ser Gly Val Gly Lys Lys Gly Lys Gln Pro Ala Arg
          20          25          30
Lys Arg Leu Asn Phe Asp Asp Glu Pro Gly Ala Gly Asp Gly Pro Pro
          35          40          45
Pro Glu Gly Pro Ser Ser Gly Ala Met Ser Thr Glu Thr Glu Met Arg
          50          55          60
Ala Ala Ala Gly Gly Asn Gly Gly Asp Ala Gly Gln Gly Ala Glu Gly
65          70          75          80

```

Val	Gly	Asn	Ala	Ser	Gly	Asp	Trp	His	Cys	Asp	Ser	Thr	Trp	Ser	Glu	85	90	95
Ser	His	Val	Thr	Thr	Ser	Thr	Arg	Thr	Trp	Val	Leu	Pro	Thr	Tyr		100	105	110
Asn	Asn	His	Leu	Tyr	Leu	Arg	Leu	Gly	Ser	Ser	Asn	Ala	Ser	Asp	Thr	115	120	125
Phe	Asn	Gly	Phe	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn	Arg	Phe	130	135	140
His	Cys	His	Phe	Ser	Pro	Arg	Asp	Trp	Gln	Arg	Leu	Ile	Asn	Asn	His	145	150	155
Trp	Gly	Leu	Arg	Pro	Lys	Ser	Met	Gln	Val	Arg	Ile	Phe	Asn	Ile	Gln	165	170	175
Val	Lys	Glu	Val	Thr	Thr	Ser	Asn	Gly	Glu	Thr	Thr	Val	Ser	Asn	Asn	180	185	190
Leu	Thr	Ser	Thr	Val	Gln	Ile	Phe	Ala	Asp	Ser	Thr	Tyr	Glu	Leu	Pro	195	200	205
Tyr	Val	Met	Asp	Ala	Gly	Gln	Glu	Gly	Ser	Leu	Pro	Pro	Phe	Pro	Asn	210	215	220
Asp	Val	Phe	Met	Val	Pro	Gln	Tyr	Gly	Tyr	Cys	Gly	Leu	Val	Thr	Gly	225	230	235
Gly	Ser	Ser	Gln	Asn	Gln	Thr	Asp	Arg	Asn	Ala	Phe	Tyr	Cys	Leu	Glu	245	250	255
Tyr	Phe	Pro	Ser	Gln	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Glu	Met	Val	260	265	270
Tyr	Lys	Phe	Glu	Asn	Val	Pro	Phe	His	Ser	Met	Tyr	Ala	His	Ser	Gln	275	280	285
Ser	Leu	Asp	Arg	Leu	Met	Asn	Pro	Leu	Leu	Asp	Gln	Tyr	Leu	Trp	Glu	290	295	300
Leu	Gln	Ser	Thr	Thr	Ser	Gly	Gly	Thr	Leu	Asn	Gln	Gly	Asn	Ser	Ala	305	310	315
Thr	Asn	Phe	Ala	Lys	Leu	Thr	Lys	Thr	Asn	Phe	Ser	Gly	Tyr	Arg	Lys	325	330	335
Asn	Trp	Leu	Pro	Gly	Pro	Met	Met	Lys	Gln	Gln	Arg	Phe	Ser	Lys	Thr	340	345	350
Ala	Ser	Gln	Asn	Tyr	Lys	Ile	Pro	Gln	Gly	Arg	Asn	Asn	Ser	Leu	Leu	355	360	365
His	Tyr	Glu	Thr	Arg	Thr	Thr	Leu	Asp	Gly	Arg	Trp	Ser	Asn	Phe	Ala	370	375	380
Pro	Gly	Thr	Ala	Met	Ala	Thr	Ala	Ala	Asn	Asp	Ala	Thr	Asp	Phe	Ser	385	390	395
Gln	Ala	Gln	Leu	Ile	Phe	Ala	Gly	Pro	Asn	Ile	Thr	Gly	Asn	Thr	Thr	405	410	415
Thr	Asp	Ala	Asn	Asn	Leu	Met	Phe	Thr	Ser	Glu	Asp	Glu	Leu	Arg	Ala	420	425	430
Thr	Asn	Pro	Arg	Asp	Thr	Asp	Leu	Phe	Gly	His	Leu	Ala	Thr	Asn	Gln	435	440	445
Gln	Asn	Ala	Thr	Thr	Val	Pro	Thr	Val	Asp	Asp	Val	Asp	Gly	Val	Gly	450	455	460
Val	Tyr	Pro	Gly	Met	Val	Trp	Gln	Asp	Arg	Asp	Ile	Tyr	Tyr	Gln	Gly	465	470	475
Pro	Ile	Trp	Ala	Lys	Ile	Pro	His	Thr	Asp	Gly	His	Phe	His	Pro	Ser	485	490	495
Pro	Leu	Ile	Gly	Phe	Gly	Leu	Lys	Ser	Pro	Pro	Pro	Gln	Ile	Phe		500	505	510
Ile	Lys	Asn	Thr	Pro	Val	Pro	Ala	Asn	Pro	Ala	Thr	Thr	Phe	Ser	Pro	515	520	525
Ala	Arg	Ile	Asn	Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr	Gly	Gln	Val	Ala	530	535	540
Val	Lys	Ile	Glu	Trp	Glu	Ile	Gln	Lys	Glu	Arg	Ser	Lys	Arg	Trp	Asn	545	550	555

```

<400> 11
Met Arg Ala Ala Ala Gly Gly Asn Gly Gly Asp Ala Gly Gln Gly Ala
 1             5             10             15
Glu Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
 20             25             30
Ser Glu Ser His Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro
 35             40             45

```

Thr	Tyr	Asn	Asn	His	Leu	Tyr	Leu	Arg	Leu	Gly	Ser	Ser	Asn	Ala	Ser
50						55					60				
Asp	Thr	Phe	Asn	Gly	Phe	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn
65					70					75					80
Arg	Phe	His	Cys	His	Phe	Ser	Pro	Arg	Asp	Trp	Gln	Arg	Leu	Ile	Asn
				85					90					95	
Asn	His	Trp	Gly	Leu	Arg	Pro	Lys	Ser	Met	Gln	Val	Arg	Ile	Phe	Asn
			100					105					110		
Ile	Gln	Val	Lys	Glu	Val	Thr	Thr	Ser	Asn	Gly	Glu	Thr	Thr	Val	Ser
		115					120					125			
Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Ile	Phe	Ala	Asp	Ser	Thr	Tyr	Glu
		130				135					140				
Leu	Pro	Tyr	Val	Met	Asp	Ala	Gly	Gln	Glu	Gly	Ser	Leu	Pro	Pro	Phe
145					150					155					160
Pro	Asn	Asp	Val	Phe	Met	Val	Pro	Gln	Tyr	Gly	Tyr	Cys	Gly	Leu	Val
				165					170					175	
Thr	Gly	Gly	Ser	Ser	Gln	Asn	Gln	Thr	Asp	Arg	Asn	Ala	Phe	Tyr	Cys
			180					185					190		
Leu	Glu	Tyr	Phe	Pro	Ser	Gln	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Glu
		195					200					205			
Met	Val	Tyr	Lys	Phe	Glu	Asn	Val	Pro	Phe	His	Ser	Met	Tyr	Ala	His
		210				215					220				
Ser	Gln	Ser	Leu	Asp	Arg	Leu	Met	Asn	Pro	Leu	Leu	Asp	Gln	Tyr	Leu
225					230					235					240
Trp	Glu	Leu	Gln	Ser	Thr	Thr	Ser	Gly	Gly	Thr	Leu	Asn	Gln	Gly	Asn
				245					250					255	
Ser	Ala	Thr	Asn	Phe	Ala	Lys	Leu	Thr	Lys	Thr	Asn	Phe	Ser	Gly	Tyr
			260					265					270		
Arg	Lys	Asn	Trp	Leu	Pro	Gly	Pro	Met	Met	Lys	Gln	Gln	Arg	Phe	Ser
		275					280					285			
Lys	Thr	Ala	Ser	Gln	Asn	Tyr	Lys	Ile	Pro	Gln	Gly	Arg	Asn	Asn	Ser
		290				295					300				
Leu	Leu	His	Tyr	Glu	Thr	Arg	Thr	Thr	Leu	Asp	Gly	Arg	Trp	Ser	Asn
305					310					315					320
Phe	Ala	Pro	Gly	Thr	Ala	Met	Ala	Thr	Ala	Ala	Asn	Asp	Ala	Thr	Asp
				325					330					335	
Phe	Ser	Gln	Ala	Gln	Leu	Ile	Phe	Ala	Gly	Pro	Asn	Ile	Thr	Gly	Asn
			340					345					350		
Thr	Thr	Thr	Asp	Ala	Asn	Asn	Leu	Met	Phe	Thr	Ser	Glu	Asp	Glu	Leu
		355					360					365			
Arg	Ala	Thr	Asn	Pro	Arg	Asp	Thr	Asp	Leu	Phe	Gly	His	Leu	Ala	Thr
		370				375					380				
Asn	Gln	Gln	Asn	Ala	Thr	Thr	Val	Pro	Thr	Val	Asp	Asp	Val	Asp	Gly
385					390					395					400
Val	Gly	Val	Tyr	Pro	Gly	Met	Val	Trp	Gln	Asp	Arg	Asp	Ile	Tyr	Tyr
				405					410					415	
Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	His	Thr	Asp	Gly	His	Phe	His
			420					425					430		
Pro	Ser	Pro	Leu	Ile	Gly	Gly	Phe	Gly	Leu	Lys	Ser	Pro	Pro	Pro	Gln
		435					440					445			
Ile	Phe	Ile	Lys	Asn	Thr	Pro	Val	Pro	Ala	Asn	Pro	Ala	Thr	Thr	Phe
		450				455					460				
Ser	Pro	Ala	Arg	Ile	Asn	Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr	Gly	Gln
465					470					475					480
Val	Ala	Val	Lys	Ile	Glu	Trp	Glu	Ile	Gln	Lys	Glu	Arg	Ser	Lys	Arg
				485					490					495	
Trp	Asn	Pro	Glu	Val	Gln	Phe	Thr	Ser	Asn	Tyr	Gly	Ala	Gln	Asp	Ser
			500					505					510		
Leu	Leu	Trp	Ala	Pro	Asp	Asn	Ala	Gly	Ala	Tyr	Lys	Glu	Pro	Arg	Ala
			515				520					525			

Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
530 535

<210> 12
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
construct

<400> 12
gtggcactcc cccccctgtc gcgttcgctc gttcgctggc tcgattgggg ggggtggcagc 60
tcaaagagct gccagacgac ggccctcttg gccgtcgccc cccaatcga gccagcgaac 120
gagcgaacgc gacagggggg ggagtgccac 150

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
construct

<400> 13
ctctagcaag ggggttttgt 20

<210> 14
<211> 7
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
construct

<400> 14
agtgtgg 7

<210> 15
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
construct

<400> 15
agggtggtgat gtcattgttg atgtcattat agttgtcacg cgatagttaa tgattaacag 60
tcatgtgatg tgtgttatcc aataggatga aagcgcgcga atgagatctc gcgagacttc 120
cggggtataa aaggggtgag tgaacgagcc cgccgccca 158

<210> 16
<211> 112
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic
construct

<400> 16
gggtggattct ggggtatattc ccgcctacct gctgccgaag gtccaaccag agcttcagtg 60
ggcgtggact aacctcgaag agtataaatt ggccgccctc aatctggagg ag 112

<210> 17
<211> 169
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
construct

<400> 17
agtcaaagac ttttttgctt gggcaaaggt caaccagggt ccggtgactc acgagtttat 60
ggttcccaag aaagtggcgg gaactgagag ggcggagact tctagaaaac gccactgga 120
tgacgtcacc aataccaact ataaaagtcc ggagaagcgg gcccggtc 169

<210> 18
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
construct

<400> 18
Gly Ser Ser Asn Ala Ser Asp Thr
1 5

<210> 19
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
construct

<400> 19
Thr Thr Ser Gly Gly Thr Leu Asn Gln Gly Asn Ser Ala Thr
1 5 10

<210> 20
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
construct

<400> 20
Asn Gly Arg Ala His Ala
1 5

<210> 21

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
construct

<400> 21
Ser Ile Gly Tyr Pro Leu Pro
1 5

<210> 22
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
construct

<400> 22
Lys Phe Asn Lys Pro Phe Val Phe Leu Ile
1 5 10

<210> 23
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
construct

<400> 23
Asn Ile Ser Leu Asp Asn Pro Leu Glu Asn Pro Ser Ser Leu Phe Asp
1 5 10 15
Leu Val Ala Arg Ile Lys
20